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## RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/777,521

TIME: 14:45:54

Input Set : N:\Cr3\RULE60\10777521.raw.txt

Output Set: N:\CRF4\08302004\J777521.raw

## SEQUENCE LISTING

## 1 (1) GENERAL INFORMATION:

(i) APPLICANT: Adema, Gosse Jan

Meygaard, Linde

Gorman, Daniel M.

McClanahan, Terrill K.

Zurawski, Sandra M.

Zurawski, Gerard

Lanier, Lewis L.

Phillips Jr., Joseph H.

(ii) TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;  
Related Reagents

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute

(B) STREET: 901 California Avenue

(C) CITY: Palo Alto

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/777,521

(B) FILING DATE: 11-Feb-2004

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/546,049

(B) FILING DATE: 10-Apr-2000

(A) APPLICATION NUMBER: US/08/985,950

(B) FILING DATE: 05-DEC-1997

(A) APPLICATION NUMBER: US 60/041,279

(B) FILING DATE: 21-MARCH-1997

(A) APPLICATION NUMBER: US 60/033,181

(B) FILING DATE: 16-DEC-1996

(A) APPLICATION NUMBER: US 60/032,252

(B) FILING DATE: 06-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.

(B) REGISTRATION NUMBER: 34,090

(C) REFERENCE/DOCKET NUMBER: DX0670K

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43      (ix) TELECOMMUNICATION INFORMATION:
44          (A) TELEPHONE: (650)852-9196
45          (B) TELEFAX: (650)496-1204
46 (2) INFORMATION FOR SEQ ID NO: 1:
47     (i) SEQUENCE CHARACTERISTICS:
48         (A) LENGTH: 1249 base pairs
49         (B) TYPE: nucleic acid
50         (C) STRANDEDNESS: single
51         (D) TOPOLOGY: linear
52     (ii) MOLECULE TYPE: cDNA
53     (ix) FEATURE:
54         (A) NAME/KEY: CDS
55         (B) LOCATION: 154..1062
56     (ix) FEATURE:
57         (A) NAME/KEY: mat_peptide
58         (B) LOCATION: 211..1062
59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60     GTTTGGGGGAA GGCTCCTGGC CCCCACAGCC CTCTTCGGAG CCTGAGCCCG GCTCTCCTCA      60
61     CTCACCTCAA CCCCCAGGCG GCCCCTCCAC AGGGCCCCCTC TCCTGCCTGG ACGGCTCTGC      120
62     TGGTCTCCCC GTCCCCTGGA GAAGAACAAG GCC ATG GGT CGG CCC CTG CTG CTG      174
63                                     Met Gly Arg Pro Leu Leu Leu
64                                     -19                      -15
65     CCC CTA CTG CCC CTG CTG CTG CCG CCA GCA TTT CTG CAG CCT AGT GGC      222
66     Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly
67         -10                      -5                      1
68     TCC ACA GGA TCT GGT CCA AGC TAC CTT TAT GGG GTC ACT CAA CCA AAA      270
69     Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys
70         5                      10                      15                      20
71     CAC CTC TCA GCC TCC ATG GGT GGC TCT GTG GAA ATC CCC TTC TCC TTC      318
72     His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe
73         25                      30                      35
74     TAT TAC CCC TGG GAG TTA GCC ACA GCT CCC GAC GTG AGA ATA TCC TGG      366
75     Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp
76         40                      45                      50
77     AGA CGG GGC CAC TTC CAC GGG CAG TCC TTC TAC AGC ACA AGG CCG CCT      414
78     Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro
79         55                      60                      65
80     TCC ATT CAC AAG GAT TAT GTG AAC CGG CTC TTT CTG AAC TGG ACA GAG      462
81     Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu
82         70                      75                      80
83     GGT CAG AAG AGC GGC TTC CTC AGG ATC TCC AAC CTG CAG AAG CAG GAC      510
84     Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp
85         85                      90                      95                      100
86     CAG TCT GTG TAT TTC TGC CGA GTT GAG CTG GAC ACA CGG AGC TCA GGG      558
87     Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly
88         105                      110                      115
89     AGG CAG CAG TGG CAG TCC ATC GAG GGG ACC AAA CTC TCC ATC ACC CAG      606
90     Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln
91         120                      125                      130

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92   GCT GTC ACG ACC ACC ACC CAG AGG CCC AGC AGC ATG ACT ACC ACC TGG      654
93   Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp
94           135                      140                      145
95   AGG CTC AGT AGC ACA ACC ACC ACA ACC GGC CTC AGG GTC ACA CAG GGC      702
96   Arg Leu Ser Ser Thr Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly
97           150                      155                      160
98   AAA CGA CGC TCA GAC TCT TGG CAC ATA AGT CTG GAG ACT GCT GTG GGG      750
99   Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly
100          165                      170                      175                      180
101   GTG GCA GTG GCT GTC ACT GTG CTC GGA ATC ATG ATT TTG GGA CTG ATC      798
102   Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile
103           185                      190                      195
104   TGC CTC CTC AGG TGG AGG AGA AGG AAA GGT CAG CAG CGG ACT AAA GCC      846
105   Cys Leu Leu Arg Trp Arg Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala
106           200                      205                      210
107   ACA ACC CCA GCC AGG GAA CCC TTC CAA AAC ACA GAG GAG CCA TAT GAG      894
108   Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu
109           215                      220                      225
110   AAT ATC AGG AAT GAA GGA CAA AAT ACA GAT CCC AAG CTA AAT CCC AAG      942
111   Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys
112           230                      235                      240
113   GAT GAC GGC ATC GTA TAT GCT TCC CTT GCC CTC TCC AGC TCC ACC TCA      990
114   Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser
115           245                      250                      255                      260
116   CCC AGA GCA CCT CCC AGC CAC CGT CCC CTC AAG AGC CCC CAG AAC GAG      1038
117   Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
118           265                      270                      275
119   ACC CTG TAC TCT GTC TTA AAG GCC TAACCAATGG ACAGCCCTCT CAAGACTGAA      1092
120   Thr Leu Tyr Ser Val Leu Lys Ala
121           280
122   TGGTGAGGCC AGGTACAGTG GCGCACACCT GTAATCCCAG CTACTCTGAA GCCTGAGGCA      1152
123   GAATCAAGTG AGCCAGGAG TTCAGGGCCA GCTTTGATAA TGGAGCGAGA TGCCATCTCT      1212
124   AGTTAAAAAT ATATATTAAC AATAAAGTAA CAAATTT      1249
126 (2) INFORMATION FOR SEQ ID NO: 2:
127   (i) SEQUENCE CHARACTERISTICS:
128       (A) LENGTH: 303 amino acids
129       (B) TYPE: amino acid
130       (D) TOPOLOGY: linear
131   (ii) MOLECULE TYPE: protein
132   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
133   Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu Pro Pro
134   -19          -15          -10          -5
135   Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
136           1           5           10
137   Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
138           15          20          25
139   Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
140           30          35          40          45
141   Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser

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142				50					55					60		
143	Phe	Tyr	Ser	Thr	Arg	Pro	Pro	Ser	Ile	His	Lys	Asp	Tyr	Val	Asn	Arg
144				65					70					75		
145	Leu	Phe	Leu	Asn	Trp	Thr	Glu	Gly	Gln	Lys	Ser	Gly	Phe	Leu	Arg	Ile
146			80					85					90			
147	Ser	Asn	Leu	Gln	Lys	Gln	Asp	Gln	Ser	Val	Tyr	Phe	Cys	Arg	Val	Glu
148		95					100					105				
149	Leu	Asp	Thr	Arg	Ser	Ser	Gly	Arg	Gln	Gln	Trp	Gln	Ser	Ile	Glu	Gly
150	110					115					120				125	
151	Thr	Lys	Leu	Ser	Ile	Thr	Gln	Ala	Val	Thr	Thr	Thr	Thr	Gln	Arg	Pro
152				130						135					140	
153	Ser	Ser	Met	Thr	Thr	Thr	Trp	Arg	Leu	Ser	Ser	Thr	Thr	Thr	Thr	Thr
154			145						150					155		
155	Gly	Leu	Arg	Val	Thr	Gln	Gly	Lys	Arg	Arg	Ser	Asp	Ser	Trp	His	Ile
156			160					165					170			
157	Ser	Leu	Glu	Thr	Ala	Val	Gly	Val	Ala	Val	Ala	Val	Thr	Val	Leu	Gly
158		175					180					185				
159	Ile	Met	Ile	Leu	Gly	Leu	Ile	Cys	Leu	Leu	Arg	Trp	Arg	Arg	Arg	Lys
160	190					195					200				205	
161	Gly	Gln	Gln	Arg	Thr	Lys	Ala	Thr	Thr	Pro	Ala	Arg	Glu	Pro	Phe	Gln
162				210						215					220	
163	Asn	Thr	Glu	Glu	Pro	Tyr	Glu	Asn	Ile	Arg	Asn	Glu	Gly	Gln	Asn	Thr
164			225						230				235			
165	Asp	Pro	Lys	Leu	Asn	Pro	Lys	Asp	Asp	Gly	Ile	Val	Tyr	Ala	Ser	Leu
166			240					245					250			
167	Ala	Leu	Ser	Ser	Ser	Thr	Ser	Pro	Arg	Ala	Pro	Pro	Ser	His	Arg	Pro
168		255					260					265				
169	Leu	Lys	Ser	Pro	Gln	Asn	Glu	Thr	Leu	Tyr	Ser	Val	Leu	Lys	Ala	
170	270				275						280					

172 (2) INFORMATION FOR SEQ ID NO: 3:

173 (i) SEQUENCE CHARACTERISTICS:

174 (A) LENGTH: 376 base pairs

175 (B) TYPE: nucleic acid

176 (C) STRANDEDNESS: single

177 (D) TOPOLOGY: linear

178 (ii) MOLECULE TYPE: cDNA

179 (ix) FEATURE:

180 (A) NAME/KEY: CDS

181 (B) LOCATION: 78..374

182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

183	CCCCAGTGTC	CCTAGACAGA	GCATCCTTGC	CTTCCTGATG	GCTTTGCTGA	TCTCGCTTCC	60					
184	CTGGAGGGGAC	TCCAGCC	ATG GCT CAG GTC CTG CTT CTG CTC TCA TCA GGC	110								
185		Met	Ala	Gln	Val	Leu	Leu	Leu	Ser	Ser	Gly	
186		1			5				10			
187	TGT CTG CAT GCT GGA AAT TCA GAA AGA TAC AAC AGA AAA AAT GGC TTT	158										
188	Cys Leu His Ala Gly Asn Ser Glu Arg Tyr Asn Arg Lys Asn Gly Phe											
189		15		20		25						
190	GGG GTC AAC CAA CCT GAA CGC TGC TCT GGA GTC CAG GGT GGC TCC ATC	206										
191	Gly Val Asn Gln Pro Glu Arg Cys Ser Gly Val Gln Gly Gly Ser Ile											

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192          30          35          40
193  GAC ATC CCC TTC TCC TTC TAT TTC CCC TGG AAG TTG GCC AAG GAT CCA      254
194  Asp Ile Pro Phe Ser Phe Tyr Phe Pro Trp Lys Leu Ala Lys Asp Pro
195          45          50          55
196  CAG ATG AGC ATA GCC TGG AAA TGG AAG GAT TTC CAT GGG GAA GTC ATC      302
197  Gln Met Ser Ile Ala Trp Lys Trp Lys Asp Phe His Gly Glu Val Ile
198          60          65          70          75
199  TAC AAC TCC TCC CTG CCT TTC ATA CAT GAG CAC TTC AAG GGC CGG CTC      350
200  Tyr Asn Ser Ser Leu Pro Phe Ile His Glu His Phe Lys Gly Arg Leu
201          80          85          90
202  ATC CTG AAC TGG ACA CAG GGT CAG AC      376
203  Ile Leu Asn Trp Thr Gln Gly Gln
204          95
206 (2) INFORMATION FOR SEQ ID NO: 4:
207   (i) SEQUENCE CHARACTERISTICS:
208       (A) LENGTH: 99 amino acids
209       (B) TYPE: amino acid
210       (D) TOPOLOGY: linear
211   (ii) MOLECULE TYPE: protein
212   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
213  Met Ala Gln Val Leu Leu Leu Leu Ser Ser Gly Cys Leu His Ala Gly
214    1          5          10          15
215  Asn Ser Glu Arg Tyr Asn Arg Lys Asn Gly Phe Gly Val Asn Gln Pro
216          20          25          30
217  Glu Arg Cys Ser Gly Val Gln Gly Gly Ser Ile Asp Ile Pro Phe Ser
218          35          40          45
219  Phe Tyr Phe Pro Trp Lys Leu Ala Lys Asp Pro Gln Met Ser Ile Ala
220          50          55          60
221  Trp Lys Trp Lys Asp Phe His Gly Glu Val Ile Tyr Asn Ser Ser Leu
222          65          70          75          80
223  Pro Phe Ile His Glu His Phe Lys Gly Arg Leu Ile Leu Asn Trp Thr
224          85          90          95
225  Gln Gly Gln
227 (2) INFORMATION FOR SEQ ID NO: 5:
228   (i) SEQUENCE CHARACTERISTICS:
229       (A) LENGTH: 1279 base pairs
230       (B) TYPE: nucleic acid
231       (C) STRANDEDNESS: single
232       (D) TOPOLOGY: linear
233   (ii) MOLECULE TYPE: cDNA
234   (ix) FEATURE:
235       (A) NAME/KEY: CDS
236       (B) LOCATION: 155..1015
237   (ix) FEATURE:
238       (A) NAME/KEY: misc_feature
239       (B) LOCATION: 1247
240       (D) OTHER INFORMATION: /note= "nucleotide 1247 designated
241  C, but may be C or T"
242   (ix) FEATURE:

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**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\10777521.raw.txt

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L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:33 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)